

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,233

DATE: 05/23/2001

TIME: 16:09:29

Input Set : A:\BB1129 seq 1st.txt

Output Set: C:\CRF3\05232001\I831233.raw

3 <110> APPLICANT: E. I. du Pont de Nemours and Company  
 5 <120> TITLE OF INVENTION: Plant Glutamine Amidotransferase Homologs  
 7 <130> FILE REFERENCE: BB1129  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/831,233  
 C--> 10 <141> CURRENT FILING DATE: 2001-05-04  
 12 <150> PRIOR APPLICATION NUMBER: 60/107,275  
 13 <151> PRIOR FILING DATE: 1998-11-05  
 15 <160> NUMBER OF SEQ ID NOS: 15  
 17 <170> SOFTWARE: Microsoft Office 97  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1956  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Impatiens balsamia  
 24 <400> SEQUENCE: 1  
 25 gcacgagaag gaactggcaa gtaccaagcc acagaatggg ttcagaattc gcgcgcgctt 60  
 26 ggctggtgca ggcggagatt ctgtggtgac tttacttgat tacggtgctg gaaatgttag 120  
 27 gagtgtgagg aacgccatcc gcacacttgg atttgatatc aaagatgtgc aaaagccaga 180  
 28 ggatattcta aatgctaagc gccttatctt tcttgccgtt ggggcctttg cacctgcaat 240  
 29 ggatgttctt attcgtaaaag ggctggctga agcactctgt acttacattc agaatgatcg 300  
 30 acctttcctg ggtatatgcc tgggattgca gctactcttt gagtcaagtg aagaaaatgg 360  
 31 tccaattcaa ggtcttggct tgattcctgg acgggttggg cgttttgaat catccaatgg 420  
 32 ttttaagggtg ccacatattg gatggcatgc cttggatata aaggaagggt cagcaatttt 480  
 33 agatgatgtg ggaatcaac atgtgtattt tgttcactca tatcgagcca atgccgagga 540  
 34 caacaaagag tggatttcac ctacatgcag ctatgggtgac gattttattg catccattca 600  
 35 gaagggaaat gttcatgcag tccaatttca tcccgaagaag agtggagggtg ttggactttc 660  
 36 catattgaga agatttttga atgctgattc ctttaacaac aaaagacaga agccaatgaa 720  
 37 tggaaaggct tctaaacttg caaagagagt aattgcttgc cttgatgtga gggcaaata 780  
 38 taatggggat cttgttgtaa ccaagggaga ccaatatgat gtgagagaac gtacagaaga 840  
 39 gaatgaggtc agaaaccttg gcaagcctgt tgaacttgcg gggcagtatt atttagacgg 900  
 40 tgctgatgag gtcagcttct taaacattac tggtttccgg gacttccctc taggcgatct 960  
 41 acccatgcta caggctcttg aacgcgcac tgaacacggt tttgtgccat taactgtcgg 1020  
 42 ggggtggcatc agggatttta ctgatgcaaa tgggaaggtat tattctagtc tagaagtggc 1080  
 43 ttcagagtat ttcagatcgg gcgcccataa ggtttcgatc ggaagtgatg cagtttacac 1140  
 44 tgctgaggaa tatattaaaa ccggagtga gacaggaaag agcagcatag agcagatatc 1200  
 45 tacagtatat ggttaaccagg cagtgggtgt aagcattgat cctcgccgag tttacttgag 1260  
 46 aaaacccgat gaagtagaat ttaaagccat caaagtaagc catccagggtc caaacgggtga 1320  
 47 ggaatatgcc tggatatcgt gcactgttaa tgggtggacga gaaggagac ccacggagc 1380  
 48 ttatgaacta gctaaggctg ttgaggaact tggagctgga gaaatattat tgaactgcat 1440  
 49 tgattgtgat ggtcaaggaa aaggattcga tatagatctg atcaagctaa tatccgatgc 1500  
 50 tgtgaacatt cctgttatcg caagcagcgg tgcaggagtc gctgatcact tctccgaagt 1560  
 51 ctttaaatgaa accaacgcat ctgctgccct tgcagctggc attttccatc gcaaagaggt 1620  
 52 tccaattaag gctgttaaag agcacttggt gaaggaaggg attgaagtta gattgtaagg 1680  
 53 cgagaatcac ttggaagaaa tttcatcttg aagttcaatt ttgttacaca agagatttcc 1740  
 54 ttctttcttg gcctatgtga tttttattta tttatgtttt gctattgaat tattgttatt 1800  
 55 attatttttg catttgttat ttgaatagat ttgagttttt agaccttggt gtgtcctgtt 1860  
 56 tatctctagg ccattgtttt tggattatat acaagtgtga aattaaata ataaatcgta 1920  
 57 tgaatttatg cttttaaaaa aaaaaaaaaa aaaaaa 1956

ENTERED  
 See p. 5

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```

59 <210> SEQ ID NO: 2
60 <211> LENGTH: 558
61 <212> TYPE: PRT
62 <213> ORGANISM: Impatiens balsamia
64 <400> SEQUENCE: 2
65 His Glu Lys Glu Leu Ala Ser Thr Lys Pro Gln Asn Gly Phe Arg Ile
66 1 5 10 15
68 Arg Ala Ala Leu Ala Gly Ala Gly Gly Asp Ser Val Val Thr Leu Leu
69 20 25 30
71 Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn Ala Ile Arg Thr
72 35 40 45
74 Leu Gly Phe Asp Ile Lys Asp Val Gln Lys Pro Glu Asp Ile Leu Asn
75 50 55 60
77 Ala Lys Arg Leu Ile Phe Pro Gly Val Gly Ala Phe Ala Pro Ala Met
78 65 70 75 80
80 Asp Val Leu Ile Arg Lys Gly Leu Ala Glu Ala Leu Cys Thr Tyr Ile
81 85 90 95
83 Gln Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln Leu Leu
84 100 105 110
86 Phe Glu Ser Ser Glu Glu Asn Gly Pro Ile Gln Gly Leu Gly Leu Ile
87 115 120 125
89 Pro Gly Arg Val Gly Arg Phe Glu Ser Ser Asn Gly Leu Arg Val Pro
90 130 135 140
92 His Ile Gly Trp His Ala Leu Asp Ile Lys Glu Gly Ser Ala Ile Leu
93 145 150 155 160
95 Asp Asp Val Gly Asn Gln His Val Tyr Phe Val His Ser Tyr Arg Ala
96 165 170 175
98 Asn Ala Glu Asp Asn Lys Glu Trp Ile Ser Ser Thr Cys Ser Tyr Gly
99 180 185 190
101 Asp Asp Phe Ile Ala Ser Ile Gln Lys Gly Asn Val His Ala Val Gln
102 195 200 205
104 Phe His Pro Glu Lys Ser Gly Gly Val Gly Leu Ser Ile Leu Arg Arg
105 210 215 220
107 Phe Leu Asn Ala Asp Ser Phe Asn Asn Lys Arg Gln Lys Pro Met Asn
108 225 230 235 240
110 Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu Asp Val
111 245 250 255
113 Arg Ala Asn Asp Asn Gly Asp Leu Val Val Thr Lys Gly Asp Gln Tyr
114 260 265 270
116 Asp Val Arg Glu Arg Thr Glu Glu Asn Glu Val Arg Asn Leu Gly Lys
117 275 280 285
119 Pro Val Glu Leu Ala Gly Gln Tyr Tyr Leu Asp Gly Ala Asp Glu Val
120 290 295 300
122 Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly Asp Leu
123 305 310 315 320
125 Pro Met Leu Gln Val Leu Gln Arg Ala Ser Glu Asn Val Phe Val Pro
126 325 330 335
128 Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Asn Gly Arg
129 340 345 350

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```

131 Tyr Tyr Ser Ser Leu Glu Val Ala Ser Glu Tyr Phe Arg Ser Gly Ala
132          355          360          365
134 Asp Lys Val Ser Ile Gly Ser Asp Ala Val Tyr Thr Ala Glu Glu Tyr
135          370          375          380
137 Ile Lys Thr Gly Val Lys Thr Gly Lys Ser Ser Ile Glu Gln Ile Ser
138 385          390          395          400
140 Thr Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro Arg Arg
141          405          410          415
143 Val Tyr Leu Arg Lys Pro Asp Glu Val Glu Phe Lys Ala Ile Lys Val
144          420          425          430
146 Ser His Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr
147          435          440          445
149 Val Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala
150          450          455          460
152 Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile
153 465          470          475          480
155 Asp Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Ile Lys Leu
156          485          490          495
158 Ile Ser Asp Ala Val Asn Ile Pro Val Ile Ala Ser Ser Gly Ala Gly
159          500          505          510
161 Val Ala Asp His Phe Ser Glu Val Phe Asn Glu Thr Asn Ala Ser Ala
162          515          520          525
164 Ala Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Lys Ala
165          530          535          540
167 Val Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Leu
168 545          550          555

```

```

170 <210> SEQ ID NO: 3
171 <211> LENGTH: 587
172 <212> TYPE: DNA
173 <213> ORGANISM: Zea mays
175 <220> FEATURE:
176 <221> NAME/KEY: unsure,
177 <222> LOCATION: (495)
179 <220> FEATURE:
180 <221> NAME/KEY: unsure/
181 <222> LOCATION: (518)
183 <220> FEATURE:
184 <221> NAME/KEY: unsure/
185 <222> LOCATION: (577)
187 <220> FEATURE:
188 <221> NAME/KEY: unsure,
189 <222> LOCATION: (582)

```

```

191 <400> SEQUENCE: 3
192 aagaaaaggc ccgctagggc gccgagacag cggaacgttc tctgagtttg agcacgatct 60
193 ccccgggccc cggcgccgcc gtacgtcccc cttcggcgtc gccagccgcc tcttggtcc 120
194 ggctccttca tcgctgctc cagcgtgcct gcgtgacata agcgtcgatt gattggcgag 180
195 aaaggggacg aatgcagccg ccgttgacagg cgcagggagc aatggctaac gtcgccgcta 240
196 tctcaccgt ccctgctcc gcgggcccgc gcccgagcg gagcaaccag ccccgcggat 300
197 gcggtccgt ctccgtctcc gtctccgtcc gtgcgtctcc cggcgcaaac acggtgactc 360

```

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```

198 tgctggacta cggcgcgggg aacgtacgca gcgtagcgcaa cgcaattcgc tacctcggct 420
199 tcgacatccg cgacgtgcag agcccggarg acatcgtcgc cggcggaayg ggtagtcttt 480
W--> 200 cccggtgtcg gcgcnttcgg ctccgccatg gacgtccnca ccaggacggg catgccaaacg 540
W--> 201 cactccgtga gtacatccaa agggaacgcc ccttcnagc cncctgcc 587
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 130
205 <212> TYPE: PRT
206 <213> ORGANISM: Zea mays
208 <220> FEATURE:
209 <221> NAME/KEY: UNSURE
210 <222> LOCATION: (90) /
212 <220> FEATURE:
213 <221> NAME/KEY: UNSURE /
214 <222> LOCATION: (93)
216 <220> FEATURE:
217 <221> NAME/KEY: UNSURE /
218 <222> LOCATION: (109)
220 <220> FEATURE:
221 <221> NAME/KEY: UNSURE /
222 <222> LOCATION: (115)
224 <220> FEATURE:
225 <221> NAME/KEY: UNSURE /
226 <222> LOCATION: (129)
228 <400> SEQUENCE: 4
229 Met Gln Pro Pro Leu Gln Ala Gln Gly Ala Met Ala Asn Val Ala Ala
230 1 5 10 15
232 Ile Leu Thr Val Pro Cys Ser Ala Gly Arg Arg Pro Lys Arg Ser Asn
233 20 25 30
235 Gln Pro Arg Gly Cys Gly Ser Val Ser Val Ser Val Ser Val Arg Ala
236 35 40 45
238 Ser Ser Gly Ala Asn Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn
239 50 55 60
241 Val Arg Ser Val Arg Asn Ala Ile Arg Tyr Leu Gly Phe Asp Ile Arg
242 65 70 75 80
W--> 244 Asp Val Gln Ser Pro Glu Asp Ile Val Xaa Ala Glu Xaa Val Val Phe
245 85 90 95
W--> 247 Pro Gly Val Gly Ala Phe Gly Ser Ala Met Asp Val Xaa Thr Arg Thr
248 100 105 110
W--> 250 Gly Met Xaa Asn Ala Leu Arg Glu Tyr Ile Gln Arg Glu Arg Pro Phe
251 115 120 125
W--> 253 Xaa Gly
254 130
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 1084
258 <212> TYPE: DNA
259 <213> ORGANISM: Zea mays
261 <400> SEQUENCE: 5
262 actagtggta acaaaaggcg atcaatatga tgtaagagat catactagca gcaaagaggt 60
263 aagaaacctt ggcaagccag tcgatttagc aagccagtac tacatagacg gtgctgatga 120

```

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```

264 ggtcagcttc ttgaatataa ctggtttccg tgactttcca ttgggtgatt tgccaatgct 180
265 agaggtactg cgttgtgcct ctgaaaagggt ttttgtgcca cttacagttg gtgggggcat 240
266 acgagacttc acagatgcaa atggaagata ctactcaagt ttggaggtag catcagaata 300
267 tttcaggtcc ggtgctgaca aaattttcaat tggaagtgat gctgtttatg ctgctgaagc 360
268 ctttttacag actggtgtaa agacaggga aagcagcttg gagcaaactc ctagagtata 420
269 tggcaatcag gctgtagtgtg tcagtattga tcctcgacgg gtatatgtca aaagtcaaga 480
270 agatgtgcca tttaaaactg taaagggtgc cactaaagggt ccatcgggag aagaatatgc 540
271 atggtaccag tgcacagtga atggtggacg tgatagccga gctataggag catatgaact 600
272 agcgaaagct gtggaagaat tgggcgcagg agaaatactt cttactgca ttgattgtga 660
273 tggccaaggt tgtggatttg acatagattt gggttaaaatg gtttctgatg ctgtgacaat 720
274 ccctgtcatt gcgagcagtg gtgctggagc tgttcaacat ttttctgaaa tttttgagaa 780
275 aacaaatgct tctgtctgcc ttgctgctgg cattttccac cggaaagagg ttcctatact 840
276 agcagtgaag gagcatctgg tcaatgctgg tgtggagggtc aggggtgtaac agggagatcc 900
277 ttcggtttat tgaaatattc ttgtttgatg tcacaactgc tatcagttct gtttctctga 960
278 tgtcgcaact gctatcagat ctgttggtgg cagctggcag tgcataggcc cctgtcgaga 1020
279 actgcagttt ggtaataaat taataatgtg atgcttaaca gattaaaaaa aaaaaaaaaa 1080
280 aaaa 1084

```

282 &lt;210&gt; SEQ ID NO: 6

283 &lt;211&gt; LENGTH: 295

284 &lt;212&gt; TYPE: PRT

285 &lt;213&gt; ORGANISM: Zea mays

287 &lt;400&gt; SEQUENCE: 6

```

288 Leu Val Val Thr Lys Gly Asp Gln Tyr Asp Val Arg Asp His Thr Ser
289 1 5 10 15
291 Ser Lys Glu Val Arg Asn Leu Gly Lys Pro Val Asp Leu Ala Ser Gln
292 20 25 30
294 Tyr Tyr Ile Asp Gly Ala Asp Glu Val Ser Phe Leu Asn Ile Thr Gly
295 35 40 45
297 Phe Arg Asp Phe Pro Leu Gly Asp Leu Pro Met Leu Glu Val Leu Arg
298 50 55 60
300 Cys Ala Ser Glu Lys Val Phe Val Pro Leu Thr Val Gly Gly Gly Ile
301 65 70 75 80
303 Arg Asp Phe Thr Asp Ala Asn Gly Arg Tyr Tyr Ser Ser Leu Glu Val
304 85 90 95
306 Ala Ser Glu Tyr Phe Arg Ser Gly Ala Asp Lys Ile Ser Ile Gly Ser
307 100 105 110
309 Asp Ala Val Tyr Ala Ala Glu Ala Phe Leu Gln Thr Gly Val Lys Thr
310 115 120 125
312 Gly Lys Ser Ser Leu Glu Gln Ile Ser Arg Val Tyr Gly Asn Gln Ala
313 130 135 140
315 Val Val Val Ser Ile Asp Pro Arg Arg Val Tyr Val Lys Ser Gln Glu
316 145 150 155 160
318 Asp Val Pro Phe Lys Thr Val Lys Val Ser Thr Lys Gly Pro Ser Gly
319 165 170 175
321 Glu Glu Tyr Ala Trp Tyr Gln Cys Thr Val Asn Gly Gly Arg Asp Ser
322 180 185 190
324 Arg Ala Ile Gly Ala Tyr Glu Leu Ala Lys Ala Val Glu Glu Leu Gly
325 195 200 205
327 Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp Cys Asp Gly Gln Gly Cys

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Input Set : A:\BB1129 seq 1st.txt

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L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:200 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:201 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:247 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:250 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:253 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:451 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:453 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:454 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:455 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:456 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:457 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:458 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:502 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:508 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:511 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:585 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:587 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:588 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:589 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:590 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:591 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:615 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:663 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:697 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14  
L:697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14